Table 4. Tumorigenic properties of CRC cells based on CD166 expression, in combination with EpCAM and/or CD44

Experiment number	Tumor source*		Lin^- sorted populations†	Cell dose	Tumor take‡	*P*§
1	UM#4	*m6*	$CD44^+/CD166^+$	1,000	**3/5**	
			$CD44^-/CD166^+$	1,000	0/5	
			$CD44^+/CD166^-$	1,000	0/2	
			$CD44^-/CD166^-$	10,000	0/5	0.0005
2	UM#4	*m6*	$CD44^+/CD166^+$	1,000	**3/5**	
			$CD44^-/CD166^+$	1,000	1/5	
			$CD44^+/CD166^-$	1,000	0/5	
			$CD44^-/CD166^-$	10,000	0/5	0.0016
3	SU29	*primary*	$EpCAM^{high}/CD166^+$	4,000	**3/5**	
			all the rest (mainly $EpCAM^{low}/CD166^-$)	4,000	0/5	*n.s.* (0.1250)
4	OMP-C8	*primary*	$EpCAM^+/CD44^+/CD166^+$	150	**1/2**	
			$EpCAM^+/CD44^+/CD166^-$	150	0/2	
			$EpCAM^+/CD44^-$	450	0/2	*n.s.* (0.2308)

*For each experiment, the *in vivo* serial passage of the tumor xenograft used as source for cancer cell purification is reported as follows: *m1*, first round of tumors obtained from primary tumor engraftment; *m2*, second round of tumors obtained from engraftment of *m1*; *m3*, third round of tumors obtained from engraftment of *m2*; and so on progressively; *primary*, primary tumor directly harvested from a surgical specimen.

†All sorted populations are to be considered as negative for expression of nonepithelial lineage markers (Lin^-; see *Materials and Methods*).

‡Tumor take is reported as number of tumors obtained/number of injections; tumor take is considered unsuccessful when no tumor mass is visible after 5 months follow-up.

§For each individual experiment, the *P* value indicates the probability of observing identical results as a matter of chance and is calculated using a hypergeometric distribution (see *SI Materials and Methods*). *n.s.*, not significant, indicates *P* values that do not reach statistical significance.